

GenAlEx 6.5 Release History, Improvements and Bug Fixes

Warning for Mac Users: Although early releases of Office 2016 are available for the Macintosh, current releases by Microsoft do not yet offer full Visual Basic for Applications (VBA) functionality, which is required to run GenAlEx within Excel. Therefore, for the time being you will need to continue to run GenAlEx in Excel 2011. Please note that this is a general issue for all VBA packages, and beyond our control. We apologise for any inconvenience.

GenAlEx 6.502 – Sep 6, 2015

- This release offers new extensions to the Shannon Diversity Analysis options initially released in GenAlEx 6.5. This update is provided to coincide with the forthcoming publication of Smouse et al. [1], which describes in detail this new Shannon Analysis. The *Shannon->Diversity Partition* option (formerly called Partition) allows estimates of *Alpha*, *Gamma* and *Beta Diversity*, as well as [0,1] Scaled *Divergence* and *Overlap*. A unique three level partition option for apportioning diversity among regions, among populations, and within populations is presented in the Shannon Statistics Summary Table, which is analogous to an AMOVA Summary Table. Although, traditional statistical testing is by means of the log-likelihood ratio G-test, which is approximately chi-square-distributed for large sample sizes, here, we offer an alternative (random permutation) test. If G-test and chi-square probability values are required they can be obtained via the Shannon Pairwise option that implements the closely related methods of Sherwin et al. (see above)[2].

GenAlEx 6.501 – June 20, 2013

- This release offers extensions to the *Check Raw Data* and *Check Matrix* option and new *Check Raw Data Color* and *Check Matrix Color* options. These provide users with a powerful tool for tracking problems within their data that may prevent GenAlEx from running.
- Within G-Statistics the Step-by-Step option has now been enabled.
- Within AMOVA an option to estimate standardized pairwise *F'st* has been enabled.
- Within Spatial analysis routines, bootstrap means and errors are now only reported when the number of pairwise comparisons for the distance class in question is >5.
- Users can now launch the GenAlEx home and download pages directly via the *Options* menu.
- Across GenAlEx we have improved the information provided when users encounter an error.
- Improved error trapping has been enabled for the G-statistics routine. Minor changes to the labelling and format of outputs have also been implemented.
- A critical *PCoA* bug in the reporting of the percentage variation explained by the first three axes has been fixed in this release.

For more detailed information about these changes please see the *Read Me GenAlEx 6.501*

GenAlEx 6.5 – Dec 23, 2012

- Minor fixes to some outputs. Error trapping for invariant loci added to Pairwise Relatedness routine.

GenAlEx 6.5b5 – Dec 14, 2012

- This version offers two new Data menu options, *Check Raw Data* and *Check Matrix*. These allow users to check GenAlEx formatted data and distance matrices for empty and non-numeric values that can prevent genetic analyses from being run.
- Another new feature, *H-individual*, is added under the Multilocus menu. H-individual allows the calculation of the proportion of loci that are heterozygous for each individual.
- Reporting of the probabilities estimated via the specialized permute option under a regional AMOVA are now output side by side with the probabilities estimated by the standard permute. See GenAlEx 6.5 Appendix 1 for more details on how these two permutational methods differ.
- Improved the outputs for Multiple Frequency Distributions (via Freq Dists of Cols).

- Fixed a bug that caused Genepop import to fail when blank lines existed after the data. Note Genepop files for import must be saved in the Windows Default text format.
- Minor fixes to labels, dialog boxes etc.

GenALEx 6.5b4 – Dec 5, 2012

- This version improves the error trapping for the *G-statistics* and *Shannon* analysis. Prior to this release, data sets with invariant loci in some populations (but not all) triggered an error that prevented the analysis from being run. Similarly, when multiple invariant loci were included, the bootstrap estimates of variance for G-statistics sometime triggered an error.
- Error trapping is also improved for the Disequilibrium - Paired Biallelic LD routines. In this case, some data sets containing locus pairs with D very close to zero failed to run. In such cases, slightly negative Chi-squared values may be encountered which triggered an Excel Function error.
- Parameters options Regions + Pops from Cols1+2, Regions+Pops from Range were completed.
- Minor labelling errors for the AMOVA routine were fixed when the option 'Supress Individual Analysis' was chosen.
- Default settings for #Permutations is now set to 999. This is the setting recommended for research, while 99 is the setting recommended for teaching. Note that on slower computers with larger AMOVA analysis, you may wish to first test your data with the number of permutations set to zero.

GenALEx 6.5b3 – Aug 30, 2012

- A recompiled 6.5b3 dated Aug 30, 2012 was released to fix a bug in the reporting of PhiPR probability values in the Hierarchical AMOVA routine.
- For simplicity the file name 6.5b3 was retained.

GenALEx 6.5b3 – Aug 29, 2012

- Enables the new Shannon Partition option

GenALEx 6.5b2 – June 15, 2012

- Now handles monomorphic loci in G-statistics which previously caused an error
- Added Jackknife and Bootstrap estimates of SE and 95% CI, respectively, across loci for G-statistics, when more than 5 loci
- Fixed a bug when all pairwise G-statistics were output for all loci, where only the total (not individual locus) values were output for G'stH, G'stC and Dest
- Now checks for more than 2 alleles in the Paired Biallelic LD option and warns users.
- Minor fixes to labels, dialog boxes etc.

GenALEx 6.5b1 – June 1, 2012

- First beta release of GenALEx 6.5

References

1. Smouse, PE, et al. 2015. *An informational diversity framework, illustrated with sexually deceptive orchids in early stages of speciation*. Molecular Ecology Resources, In press: DOI 10.1111/1755-0998.12422.
2. Sherwin, W, et al. 2006. *Measurement of biological information with applications from genes to landscapes* Molecular Ecology **15**, 2857-2869.